

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Godowski, Paul J.
Gurney, Austin L.
- (ii) TITLE OF INVENTION: Tie Ligands
- 10 (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 30 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Dreger, Ginger R.
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: P1130
- 35 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 650/225-3216

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2290 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTGAGGGG AGGCCCCGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50
CTGGTGGGTG GAGAGAAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100
ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150
AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200
GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250
GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300
CCGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350
GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400
CAGGCTGCCC CGCTGACGGC CAGGGTGAAG CATGTGAGGA GCCGCCCCGG 450
AGCCAAGCAG GAGGGAAGAG GCTTTCATAG ATTCTATTCA CAAAGAATAA 500
CCACCATTTT GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550
TCGGA CTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTTT 600
GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTTACC TAAACAGGTA 650

65

PATENT DOCKET P1130

CAAGCGGGCG GCGGAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700

CCCAGCAGCG GGTCACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750

5 GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTCAACAA 800

TGAGCTGCTC AAGCAGAAGC GGCAGATCGA GACGCTGCAG CAGCTGGTGG 850

AGGTGGACGG CGGCATTGTG AGCGAGGTGA AGCTGCTGCG CAAGGAGAGC 900

10 CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950

GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAACA 1000

15 GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050

GACCTGGAGC ACAAGTACCA GCACCTGGCC AACTGGCCC ACAACCAATC 1100

AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150

20 GGCCCGTCCC CCAGCCACCC CCCGCTGCCC CGCCCCGGGT CTACCAACCA 1200

CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250

25 TGACCAGAAC CTGAAGGTGC TGCCACCCCC TCTGCCCACT ATGCCCACTC 1300

TCACCAGCCT CCCATCTTCC ACCGACAAGC CGTCGGGCCC ATGGAGAGAC 1350

TGCCTGCAGG CCCTGGAGGA TGGCCACGAC ACCAGCTCCA TCTACCTGGT 1400

30 GAAGCCGGAG AACACCAACC GCCTCATGCA GGTGTGGTGC GACCAGAGAC 1450

ACGACCCCGG GGGCTGGACC GTCATCCAGA GACGCCTGGA TGGCTCTGTT 1500

35 AACTTCTTCA GGAAGTGGGA GACGTACAAG CAAGGGTTTG GGAACATTGA 1550

CGGCGAATAC TGGCTGGGCC TGGAGAACAT TTAAGTGGCTG ACGAACCAAG 1600

66

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GCAACTACAA ACTCCTGGTG ACCATGGAGG ACTGGTCCGG CCGCAAAGTC 1650

TTTGCAGAAT ACGCCAGTTT CCGCCTGGAA CCTGAGAGCG AGTATTATAA 1700

5 GCTGCGGCTG GGGCGCTACC ATGGCAATGC GGGTGACTCC TTTACATGGC 1750

ACAACGGCAA GCAGTTCACC ACCCTGGACA GAGATCATGA TGTCTACACA 1800

10 GGAAACTGTG CCCACTACCA GAAGGGAGGC TGGTGGTATA ACGCCTGTGC 1850

CCACTCCAAC CTCAACGGGG TCTGGTACCG CGGGGGCCAT TACCGGAGCC 1900

GCTACCAGGA CGGAGTCTAC TGGGCTGAGT TCCGAGGAGG CTCTTACTCA 1950

15 CTCAAGAAAG TGGTGATGAT GATCCGACCG AACCCCAACA CCTTCCACTA 2000

AGCCAGCTCC CCCTCCTGAC CTCTCGTGGC CATTGCCAGG AGCCCACCCT 2050

20 GGTCACGCTG GCCACAGCAC AAAGAACAAC TCCTCACCAG TTCATCCTGA 2100

GGCTGGGAGG ACCGGGATGC TGGATTCTGT TTTCCGAAGT CACTGCAGCG 2150

GATGATGGAA CTGAATCGAT ACGGTGTTTT CTGTCCCTCC TACTTTCCTT 2200

25 CACACCAGAC AGCCCCTCAT GTCTCCAGGA CAGGACAGGA CTACAGACAA 2250

CTCTTTCTTT AAATAAATTA AGTCTCTACA ATAAAAAAAA 2290

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala
1				5					10					15
Ala	Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr
				20					25					30
Glu	Glu	Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys
				35					40					45
Arg	Ala	Gly	Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val
				50					55					60
Pro	Gln	Gln	Arg	Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu
				65					70					75
Pro	Glu	Val	Leu	Leu	Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu
				80					85					90
Leu	Leu	Asn	Asn	Glu	Leu	Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr
				95					100					105
Leu	Gln	Gln	Leu	Val	Glu	Val	Asp	Gly	Gly	Ile	Val	Ser	Glu	Val
				110					115					120
Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr
				125					130					135
Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp
				140					145					150
Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn	Arg	Ile	Leu	Asn	Gln
				155					160					165
Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr	Lys	Asp	Leu	Glu
				170					175					180

PATENT DOCKET P1130

His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn Gln Ser Glu
185 190 195

5 Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro Ser Ala
200 205 210

Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val Tyr
215 220 225

10 Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
230 235 240

Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu
245 250 255

15 Pro Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys
260 265 270

20 Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
275 280 285

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn
290 295 300

25 Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly
305 310 315

Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
320 325 330

30 Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly
335 340 345

35 Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln
350 355 360

PATENT DOCKET P1130

Gly Asn Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg
365 370 375

Lys Val Phe Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser
380 385 390

Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly
395 400 405

Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe Thr Thr Leu Asp
410 415 420

Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His Tyr Gln Lys
425 430 435

Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu Asn Gly
440 445 450

Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly
455 460 465

Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490 493

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3355 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

PATENT DOCKET P1130

GCAGCTGGTT ACTGCATTTTCC TCCATGTGGC AGACAGAGCA AAGCCACAAC 50

GCTTTCTCTG CTGGATTAAA GACGGCCAC AGACCAGAAC TTCCACTATA 100

5 CTACTIONAAAA TTACATAGGT GGCTTGTCAA ATTCAATTGA TTAGTATTGT 150

AAAAGGAAAA AGAAGTTCCT TCTTACAGCT TGGATTCAAC GGTCCAAAAAC 200

AAAAATGCAG CTGCCATTAA AGTCTCAGAT GAACAAACTT CTACACTGAT 250

10 TTTTAAAAATC AAGAATAAGG GCAGCAAGTT TCTGGATTCA CTGAATCAAC 300

AGACACAAAA AGCTGGCAAT ATAGCAACTA TGAAGAGAAA AGCTACTAAT 350

15 AAAATTAACC CAACGCATAG AAGACTTTTT TTTCTCTTCT AAAAACAACT 400

AAGTAAAGAC TTAAATTTAA ACACATCATT TTACAACCTC ATTTCAAAAT 450

GAAGACTTTT ACCTGGACCC TAGGTGTGCT ATTCTTCCTA CTAGTGGACA 500

20 CTGGACATTG CAGAGGTGGA CAATTCAAAA TTAATAAAT AAACCAGAGA 550

AGATACCCTC GTGCCACAGA TGGTAAAGAG GAAGCAAAGA AATGTGCATA 600

25 CACATTCCTG GTACCTGAAC AAAGAATAAC AGGGCCAATC TGTGTCAACA 650

CCAAGGGGCA AGATGCAAGT ACCATTAAAG ACATGATCAC CAGGATGGAC 700

CTTGAAAACC TGAAGGATGT GCTCTCCAGG CAGAAGCGGG AGATAGATGT 750

30 TCTGCAACTG GTGGTGGATG TAGATGGAAA CATTGTGAAT GAGGTAAAGC 800

TGCTGAGAAA GGAAAGCCGT AACATGAACT CTCGTGTTAC TCAACTCTAT 850

35 ATGCAATTAT TACATGAGAT TATCCGTAAG AGGGATAATT CACTTGAACT 900

TTCCCAACTG GAAAACAAAA TCCTCAATGT CACCACAGAA ATGTTGAAGA 950

PATENT DOCKET P1130

TGGCAACAAG ATACAGGGAA CTAGAGGTGA AATACGCTTC CTTGACTGAT 1000

CTTGTCAATA ACCAATCTGT GATGATCACT TTGTTGGAAG AACAGTGCTT 1050

5 GAGGATATTT TCCCGACAAG ACACCCATGT GTCTCCCCCA CTTGTCCAGG 1100

TGGTGCCACA ACATATTCCT AACAGCCAAC AGTATACTCC TGGTCTGCTG 1150

GGAGGTAACG AGATTCAGAG GGATCCAGGT TATCCCAGAG ATTTAATGCC 1200

10 ACCACCTGAT CTGGCAACTT CTCCCACCAA AAGCCCTTTC AAGATACCAC 1250

CGGTAACTTT CATCAATGAA GGACCATTCA AAGACTGTCA GCAAGCAAAA 1300

15 GAAGCTGGGC ATTCGGTCAG TGGGATTTAT ATGATTAAAC CTGAAAACAG 1350

CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTTGGAC CCTGGGGGTT 1400

GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450

20 TGGGAAAATT ATAAGAAAGG GTTTGGAAAC ATTGACGGAG AATACTGGCT 1500

TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550

25 TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600

AGCTTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650

TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAAACAAT 1700

30 TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCAC 1750

TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800

35 TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850

TTTTCTGGGC CGAATACAGA GCGGGTCAT ACTCCTTAAG AGCAGTTCAG 1900

PATENT DOCKET P1130

ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACTCGCCA ATTTAAATGA 1950

CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000

5 ATTACTTGGC ACAATTTATT TCTACACAGA AAGTTTTTAA AATGAATTTT 2050

ACCGTAACTA TAAAAGGGAA CCTATAAATG TAGTTTCATC TGTCGTCAAT 2100

10 TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTTT AAAAATTATG 2150

TTGACTAAAT ACAAAGTTTG TTTTCTAAAA TGTAAATATT TGCCACAATG 2200

TAAAGCAAAT CTTAGCTATA TTTTAAATCA TAAATAACAT GTTCAAGATA 2250

15 CTTAACAATT TATTTAAAAT CTAAGATTGC TCTAACGTCT AGTGAAAAAA 2300

ATATTTTTTA AATTTTCAGCC AAATAATGCA TTTTATTTTA TAAAAATACA 2350

GACAGAAAAT TAGGGAGAAA CTTCTAGTTT TGCCAATAGA AAATGTTCTT 2400

20 CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450

GATTAAATCT GAATTCCTAA TAATATATCC TATGCTGATT TTCCCAAAAC 2500

25 ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAAACCC 2550

AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600

TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAAT 2650

30 CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700

ACAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

35 TTTATTATTA CTTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800

AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850

AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900

CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950

5 CCACAGGGGC ATAGCTTAGT CCAAAGTCT AATTTCATTT TACAGTGTAT 3000

GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAAC 3050

TTACTAGTGA CTTTCTGGAA CAATTTCTTT TCAGGAATAC ATATTCAGT 3100

10 CTTAGAGGTG ACCTTGCTTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150

TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200

15 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250

GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300

20 AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350

AAAAA 3355

(2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Thr Phe Thr Trp Thr Leu Gly Val Leu Phe Phe Leu Leu
1 5 10 15

35 Val Asp Thr Gly His Cys Arg Gly Gly Gln Phe Lys Ile Lys Lys
20 25 30

PATENT DOCKET P1130

Ile Asn Gln Arg Arg Tyr Pro Arg Ala Thr Asp Gly Lys Glu Glu
35 40 45

5 Ala Lys Lys Cys Ala Tyr Thr Phe Leu Val Pro Glu Gln Arg Ile
50 55 60

Thr Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr
65 70 75

10 Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp
80 85 90

Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val
95 100 105

15 Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg
110 115 120

20 Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met
125 130 135

Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu
140 145 150

25 Leu Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met
155 160 165

Leu Lys Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala
170 175 180

30 Ser Leu Thr Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu
185 190 195

35 Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser Arg Gln Asp Thr His
200 205 210

75

PATENT DOCKET P1130

Val Ser Pro Pro Leu Val Gln Val Val Pro Gln His Ile Pro Asn
215 220 225

Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn Glu Ile Gln
230 235 240

Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro Asp Leu
245 250 255

Ala Thr Ser Pro Thr Lys Ser Pro Phe Lys Ile Pro Pro Val Thr
260 265 270

Phe Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu
275 280 285

Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
290 295 300

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro
305 310 315

Gly Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn
320 325 330

Phe Phe Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile
335 340 345

Asp Gly Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser
350 355 360

Asn Gln Asp Asn Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser
365 370 375

Asp Lys Lys Val Tyr Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro
380 385 390

PATENT DOCKET P1130

Glu Ser Glu Phe Tyr Arg Leu Arg Leu Gly Thr Tyr Gln Gly Asn
395 400 405

Ala Gly Asp Ser Met Met Trp His Asn Gly Lys Gln Phe Thr Thr
410 415 420

Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn Cys Ala His Phe
425 430 435

His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
440 445 450

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln
455 460 465

Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu
470 475 480

Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
485 490 491

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCAGAGG CCCCACTGGA CCCTCGGCTC TTCCTTGGAC TTCTTGTGTG 50

TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100

TGGGAAGGTC CGCCGCGATG GGGAAGCCCT GGCTGCGTGC GCTACAGCTG 150

PATENT DOCKET P1130

CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200

CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250

5 GCGGCCCCGC ATCCACGCGG GCGACGCCCC AGGCCGCCAA CGCCAGCGAG 300

CTGGCGGGCGC TGCGCATGCG CGTCGGCCGC CACGAGGAGC TGTTACGCGA 350

GCTGCAGAGG CTGGCGGGCG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400

10 CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450

GCGCAGCTGC AGCACGAGGC GGGGCCCCGG GCGGGCCCCG GGGCGGATCT 500

15 GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550

ACGCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600

GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650

20 CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700

TCCTGCCGCC ACCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750

25 AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800

AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850

GTCACCCTGC GGTCCCCACC AAGCCTGTGG GCCCGTGGCA GGATTGTGCA 900

30 GAGGCCCCGC AGGCAGGCCA TGAACAGAGT GGAGTGATG AACTGCGAGT 950

GGGCCGTACG GTAGTGTCAG TATGGTGTGA GCAGCAACTG GAGGGTGGAG 1000

35 GCTGGACTGT GATCCAGCGG AGGCAAGATG GTTCAGTCAA CTTCTTCACT 1050

ACCTGGCAGC ACTATAAGGC GGGCTTTGGG CGGCCAGACG GAGAATACTG 1100

PATENT DOCKET P1130

GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150

TGCTGGTTCT CCTGGAGGAC TGGGGGGGCC GTGGAGCACG TGCCCACTAT 1200

5 GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TCGGGCTTGG 1250

CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300

10 CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350

CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400

CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450

15 GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500

GCCATGCTCA TTCGGCCCCT GAAGCTGTGA CTCTGTGTTC CTCTGTCCCC 1550

20 TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600

CCTTCTTTGT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650

ATCTGTGACC CTGGGCGCTG AAAATGGGAC CCAGGAATCC CCCCCGTCAA 1700

25 TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCATATCT CGGTTTGAGC 1750

TCATATCTTA TAATAACACA AAGTAGCCAC 1780

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Lys	Pro	Trp	Leu	Arg	Ala	Leu	Gln	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Gly	Ala	Ser	Trp	Ala	Arg	Ala	Gly	Ala	Pro	Arg	Cys	Thr	Tyr	Thr	20	25	30	
Phe	Val	Leu	Pro	Pro	Gln	Lys	Phe	Thr	Gly	Ala	Val	Cys	Trp	Ser	35	40	45	
Gly	Pro	Ala	Ser	Thr	Arg	Ala	Thr	Pro	Glu	Ala	Ala	Asn	Ala	Ser	50	55	60	
Glu	Leu	Ala	Ala	Leu	Arg	Met	Arg	Val	Gly	Arg	His	Glu	Glu	Leu	65	70	75	
Leu	Arg	Glu	Leu	Gln	Arg	Leu	Ala	Ala	Ala	Asp	Gly	Ala	Val	Ala	80	85	90	
Gly	Glu	Val	Arg	Ala	Leu	Arg	Lys	Glu	Ser	Arg	Gly	Leu	Ser	Ala	95	100	105	
Arg	Leu	Gly	Gln	Leu	Arg	Ala	Gln	Leu	Gln	His	Glu	Ala	Gly	Pro	110	115	120	
Gly	Ala	Gly	Pro	Gly	Ala	Asp	Leu	Gly	Ala	Glu	Pro	Ala	Ala	Ala	125	130	135	
Leu	Ala	Leu	Leu	Gly	Glu	Arg	Val	Leu	Asn	Ala	Ser	Ala	Glu	Ala	140	145	150	
Gln	Arg	Ala	Ala	Ala	Arg	Phe	His	Gln	Leu	Asp	Val	Lys	Phe	Arg	155	160	165	
Glu	Leu	Ala	Gln	Leu	Val	Thr	Gln	Gln	Ser	Ser	Leu	Ile	Ala	Arg	170	175	180	

PATENT DOCKET P1130

Leu Glu Arg Leu Cys Pro Gly Gly Ala Gly Gly Gln Gln Gln Val
185 190 195

Leu Pro Pro Pro Pro Leu Val Pro Val Val Pro Val Arg Leu Val
200 205 210

Gly Ser Thr Ser Asp Thr Ser Arg Met Leu Asp Pro Ala Pro Glu
215 220 225

Pro Gln Arg Asp Gln Thr Gln Arg Gln Gln Glu Pro Met Ala Ser
230 235 240

Pro Met Pro Ala Gly His Pro Ala Val Pro Thr Lys Pro Val Gly
245 250 255

Pro Trp Gln Asp Cys Ala Glu Ala Arg Gln Ala Gly His Glu Gln
260 265 270

Ser Gly Val Tyr Glu Leu Arg Val Gly Arg His Val Val Ser Val
275 280 285

Trp Cys Glu Gln Gln Leu Glu Gly Gly Gly Trp Thr Val Ile Gln
290 295 300

Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His
305 310 315

Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly
320 325 330

Leu Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu
335 340 345

Leu Val Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His
350 355 360

PATENT DOCKET P1130

Tyr Asp Gly Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu
365 370 375

Arg Leu Gly Gln Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp
380 385 390

His Asn Asp Lys Pro Phe Ser Thr Val Asp Arg Asp Arg Asp Ser
395 400 405

Tyr Ser Gly Asn Cys Ala Leu Tyr Gln Arg Gly Gly Trp Trp Tyr
410 415 420

His Ala Cys Ala His Ser Asn Leu Asn Gly Val Trp His His Gly
425 430 435

Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu
440 445 450

Phe Arg Gly Gly Ala Tyr Ser Leu Arg Lys Ala Ala Met Leu Ile
455 460 465

Arg Pro Leu Lys Leu
470

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGACGAAC CAAGGCAACT ACAAACCTCCT GGT 33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCGGCCGGA CCAGTCCTCC ATGGTCACCA GGAGTTTGTA G 41

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTGGTGAAC TGCTTGCCGT TGTGCCATGT AAA 33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGTTATCC CAGAGATTTA ATGCCACCA 29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTGGTGGGAG AAGTTGCCAG ATCAGGTGGT GGCA 34

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCACACCAT AACTGCATTG GTCCA 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTAGTTCC AGTATGGTGT GAGCAGCAAC TGGA 34

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTCCAGCCT CCACCCTCCA GTTGCT 26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCAGTCCT CCAGGAGAAC CAGCA 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2042 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150
10 ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
TTCAAAAAC TCAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
15 ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
20 CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
25 ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
30 GACTAGTATT CAAGAACCCA CAGAAATTTT TCTATCTTCC AAGCCAAGAG 700
CACCAAGAAC TACTCCCTTT CTTCA GTTGA ATGAAATAAG AAATGTAAAA 750
CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
35 TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850

PATENT DOCKET P1130

TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900

ATAGATGGAT CACAAAACCTT CAATGAAACG TGGGAGAACT ACAAATATGG 950

5 TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000

CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050

10 AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100

AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCAATG 1150

CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGA TCACAAAGCA 1200

15 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250

TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

20 CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGA GTCTCAAAAT 1350

GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400

TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450

25 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500

AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550

AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600

30 AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650

CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700

35 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750

ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAACTA GTACTCTTGT 1800

PATENT DOCKET P1130

TAAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850

TAAATGTTGT AGTATTAATT TCAAAACTAA AAATCGTCAG CACAGAGTAT 1900

5 GTGTAAAAAT CTGTAATACA AATTTTTTAAA CTGATGCTTC ATTTTGCTAC 1950

AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000

AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile
1 5 10 15

Ser Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser
20 25 30

Pro Glu Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile
35 40 45

Leu Ala Asn Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe
50 55 60

Val His Lys Thr Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu
65 70 75

Asn Ile Phe Asp Gln Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser
80 85 90

88

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Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg Arg Thr Thr Tyr Lys
 95 100 105

5 Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu
 110 115 120

Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln
 125 130 135

10 Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln
 140 145 150

Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys
 155 160 165

15 Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln
 170 175 180

20 Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln
 185 190 195

Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu
 200 205 210

25 Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr
 215 220 225

Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
 230 235 240

30 Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His
 245 250 255

35 Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe
 260 265 270

89

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His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile
275 280 285

Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu
290 295 300

Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu
305 310 315

Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val
320 325 330

Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile
335 340 345

Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu
350 355 360

His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu
365 370 375

Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly
380 385 390

His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp His
395 400 405

Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
410 415 420

Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys
425 430 435

Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu
440 445 450

Ile His Pro Thr Asp Ser Glu Ser Phe Glu
455 460